FIGURE 1A

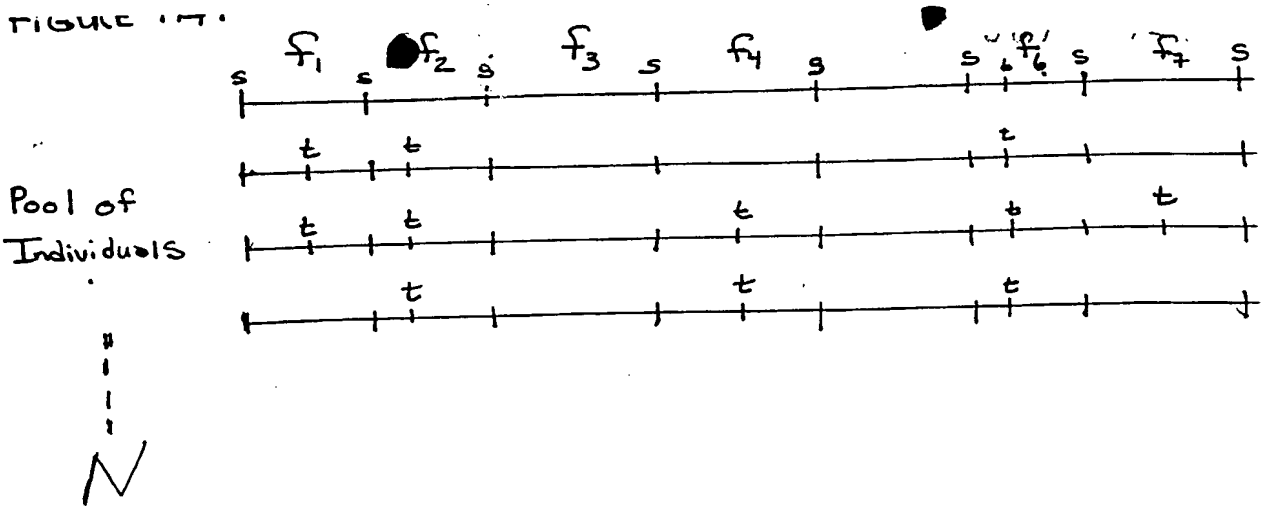


FIGURE 1B

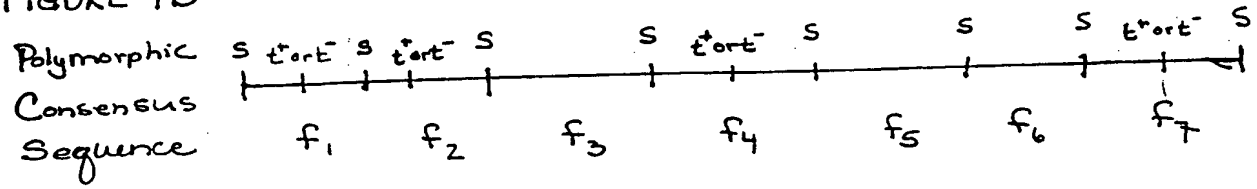


FIGURE 1C

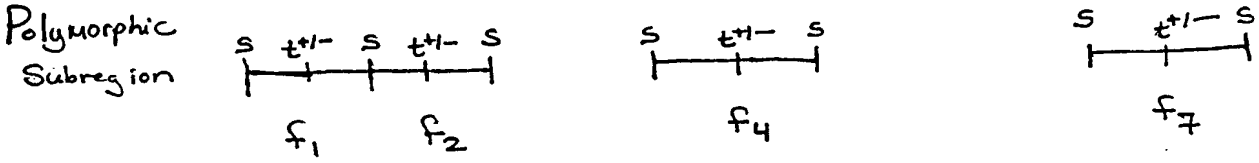
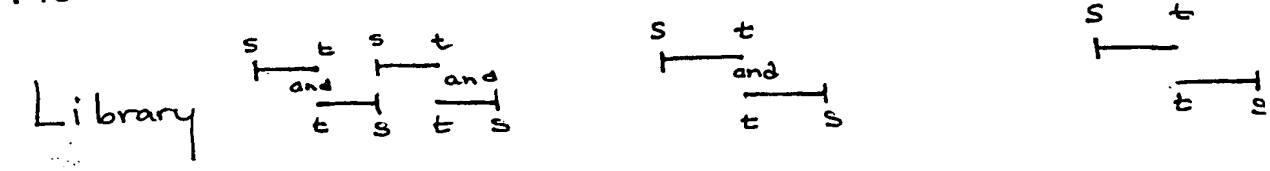


FIGURE 1D



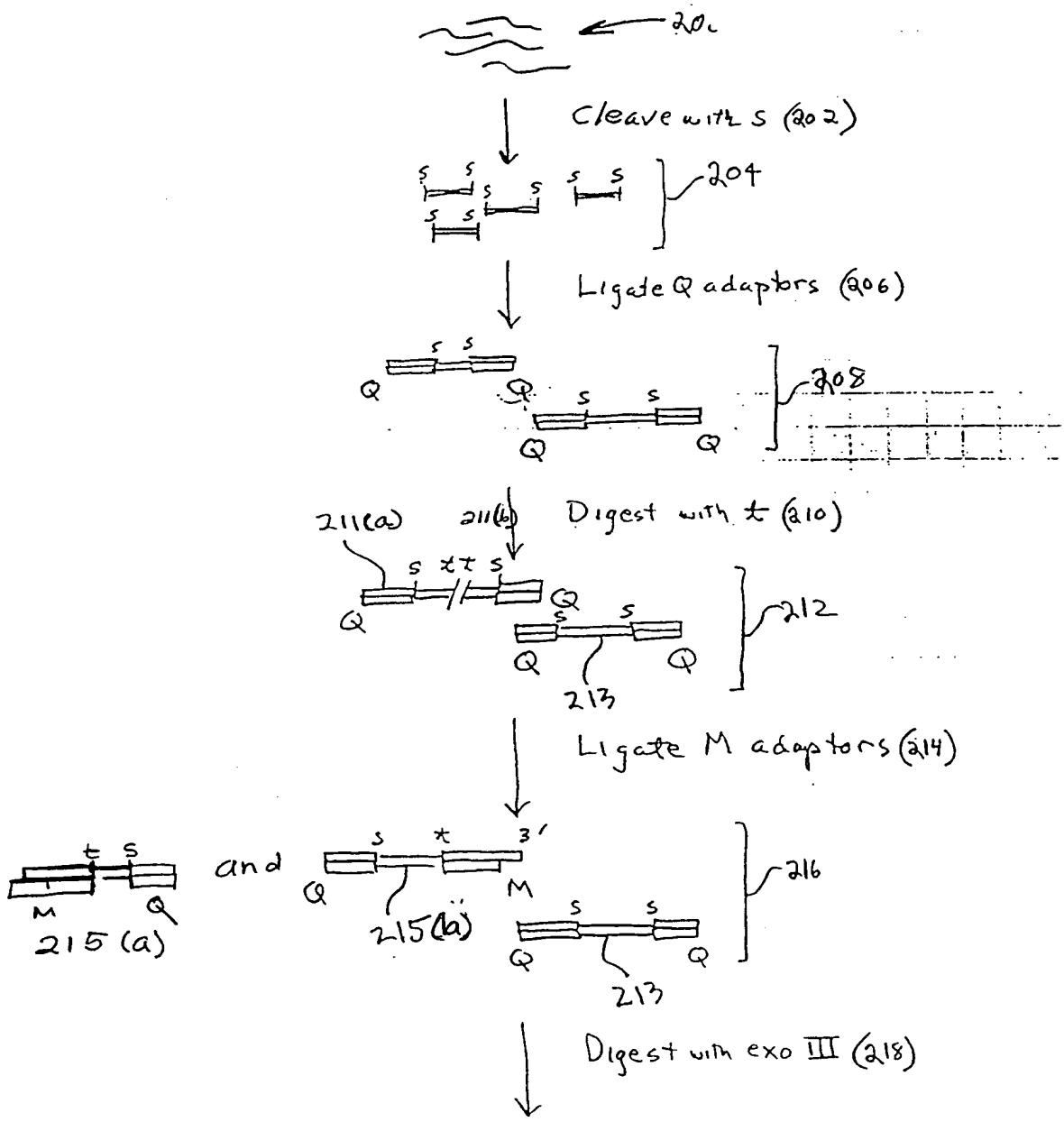

202
Cleave with S (202)
204
Ligate Q adaptors (206)
208
211(a)
211(b)
Digest with t (210)
212
213
Ligate M adaptors (214)
215(a)
and
215(b)
216
213
Digest with exo III (218)

Fig. 2A

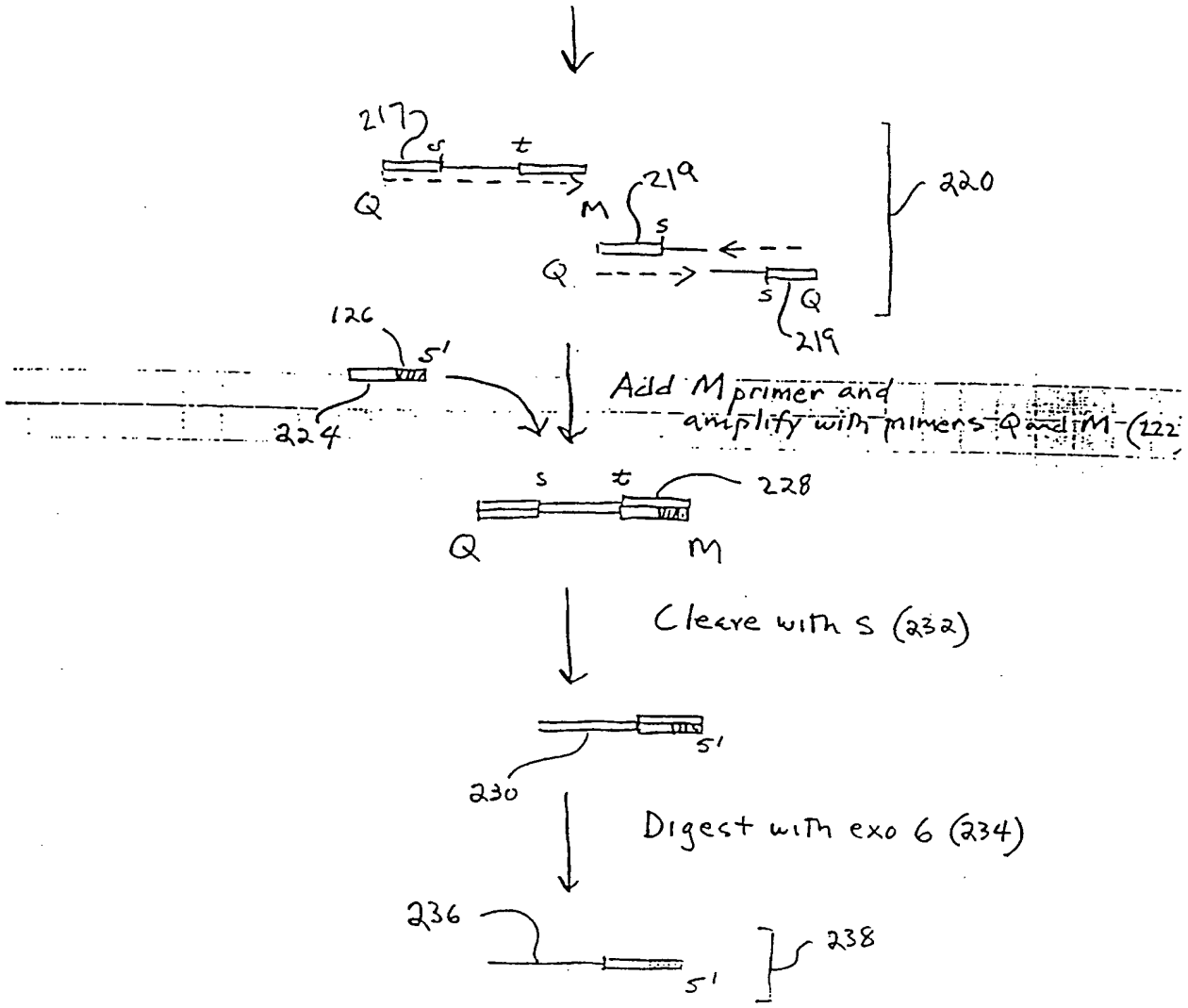

217
s
t
Q
M
219
s
220
Q
s
Q
219
126
5'
224
Add M primer and
amplify with primers Q and M (222
s
t
228
Q
M
Cleave with S (232)
5'
230
Digest with exo 6 (234)
236
5'
238

Fig 2B

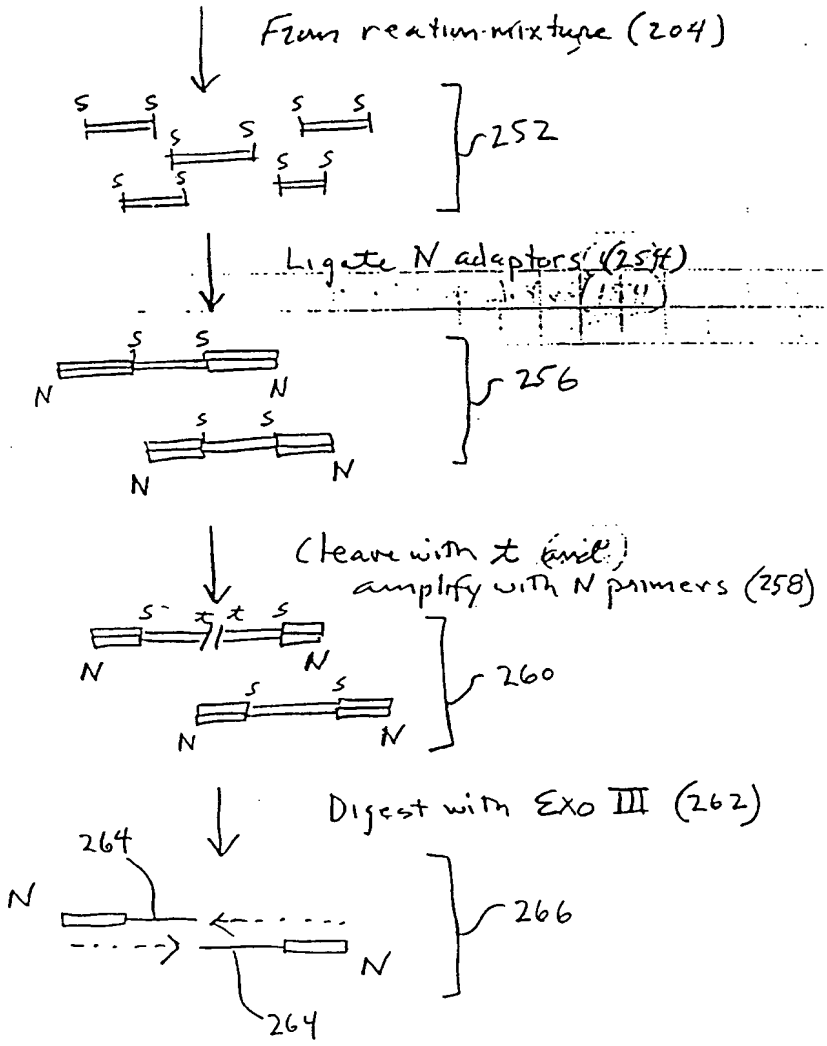

From reaction mixture (204)
252
Ligate N adaptors (254)
256
Cleave with x (and)
amplify with N primers (258)
260
Digest with Exo III (262)
264
266
264

Fig. 2E

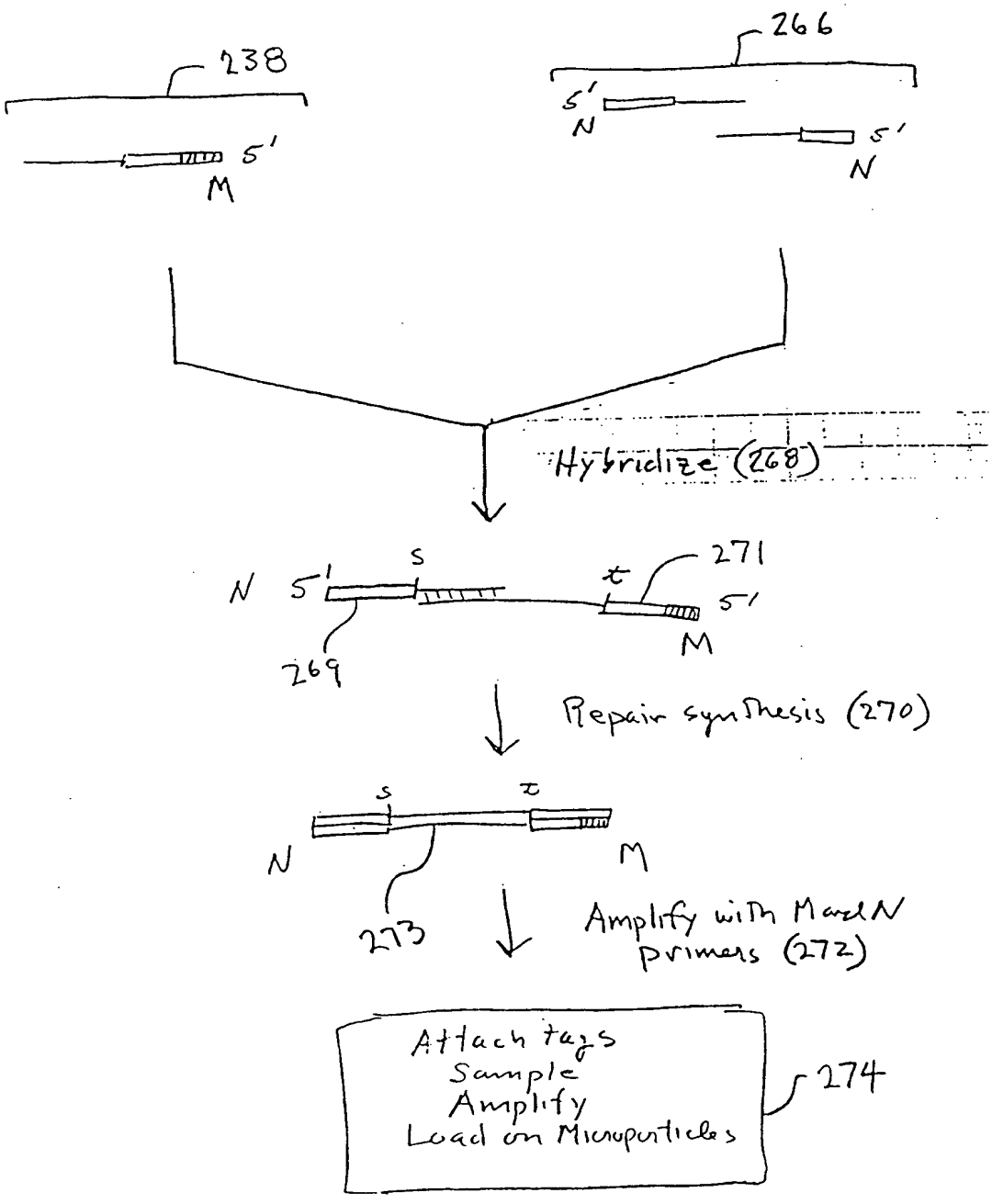

238
5'
M
266
5'
N
5'
N
Hybridize (268)
N
5'
S
271
t
5'
M
269
Repair synthesis (270)
S
t
N
M
273
Amplify with M and N primers (272)
Attach tags
Sample
Amplify
Load on Microparticles
274

Fig. 2I

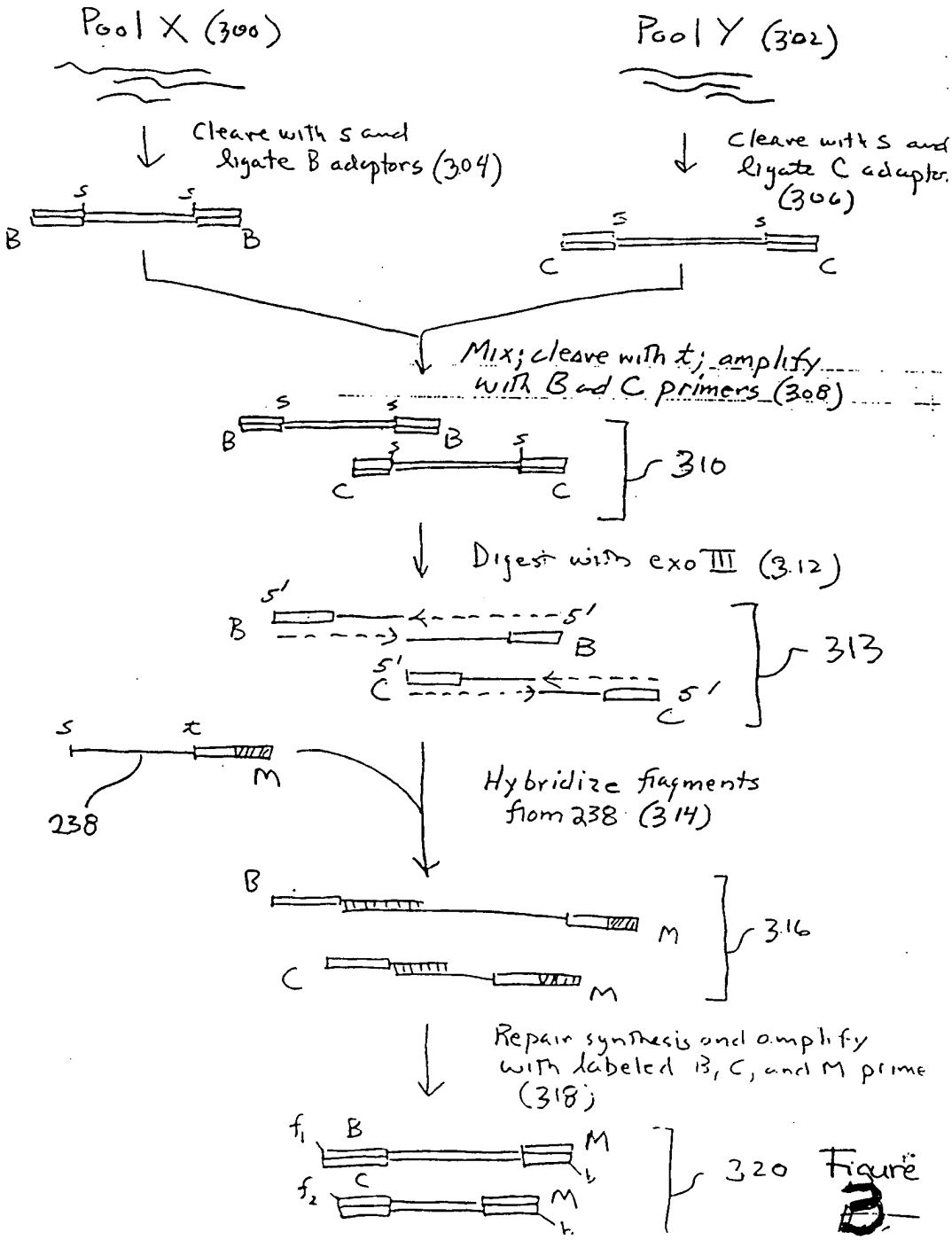

Pool X (300)
Pool Y (302)
Cleave with s and ligate B adaptors (304)
Cleave with s and ligate C adaptor (306)
Mix; cleave with t; amplify with B and C primers (308)
310
Digest with exo III (312)
313
Hybridize fragments from 238 (314)
316
Repair synthesis and amplify with labeled B, C, and M prime (318)
320

Figure 3

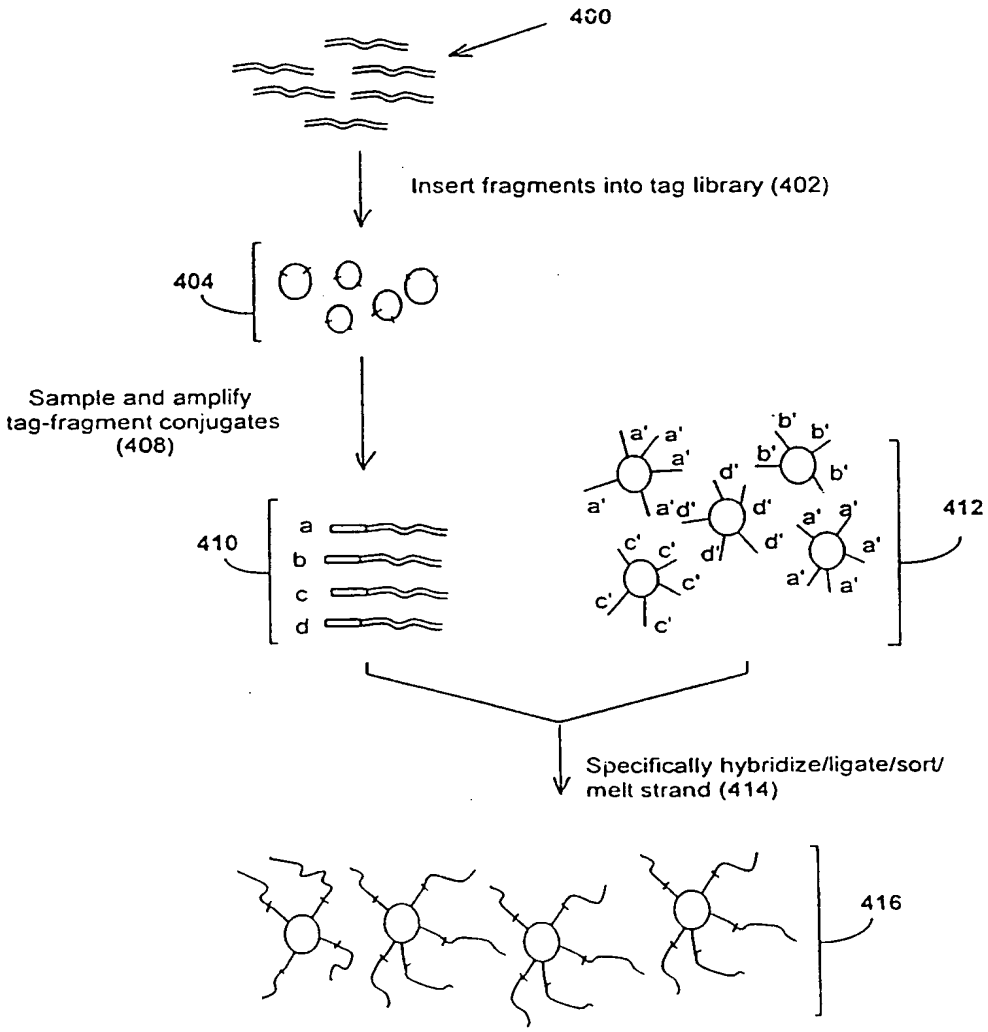

400
Insert fragments into tag library (402)
404
Sample and amplify
tag-fragment conjugates
(408)
410
a
b
c
d
412
Specifically hybridize/ligate/sort/
melt strand (414)
416

Fig. 4

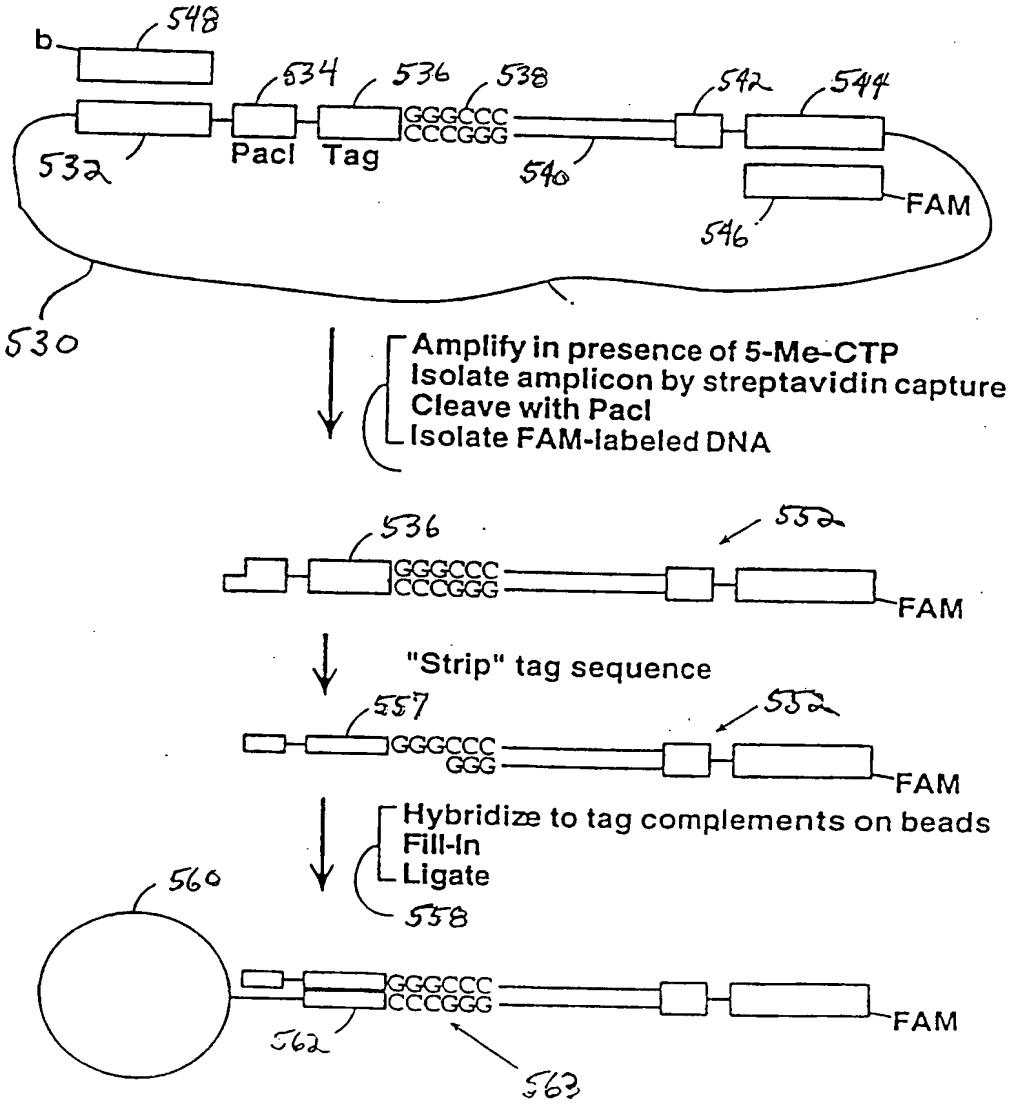

b
548
534
536
538
542
544
GGGCCC
CCCGGG
532
PacI
Tag
540
FAM
546
530
Amplify in presence of 5-Me-CTP
Isolate amplicon by streptavidin capture
Cleave with PacI
Isolate FAM-labeled DNA
536
552
GGGCCC
CCCGGG
FAM
"Strip" tag sequence
557
552
GGGCCC
GGG
FAM
Hybridize to tag complements on beads
Fill-In
Ligate
558
560
GGGCCC
CCCGGG
FAM
562
563

Fig 5A

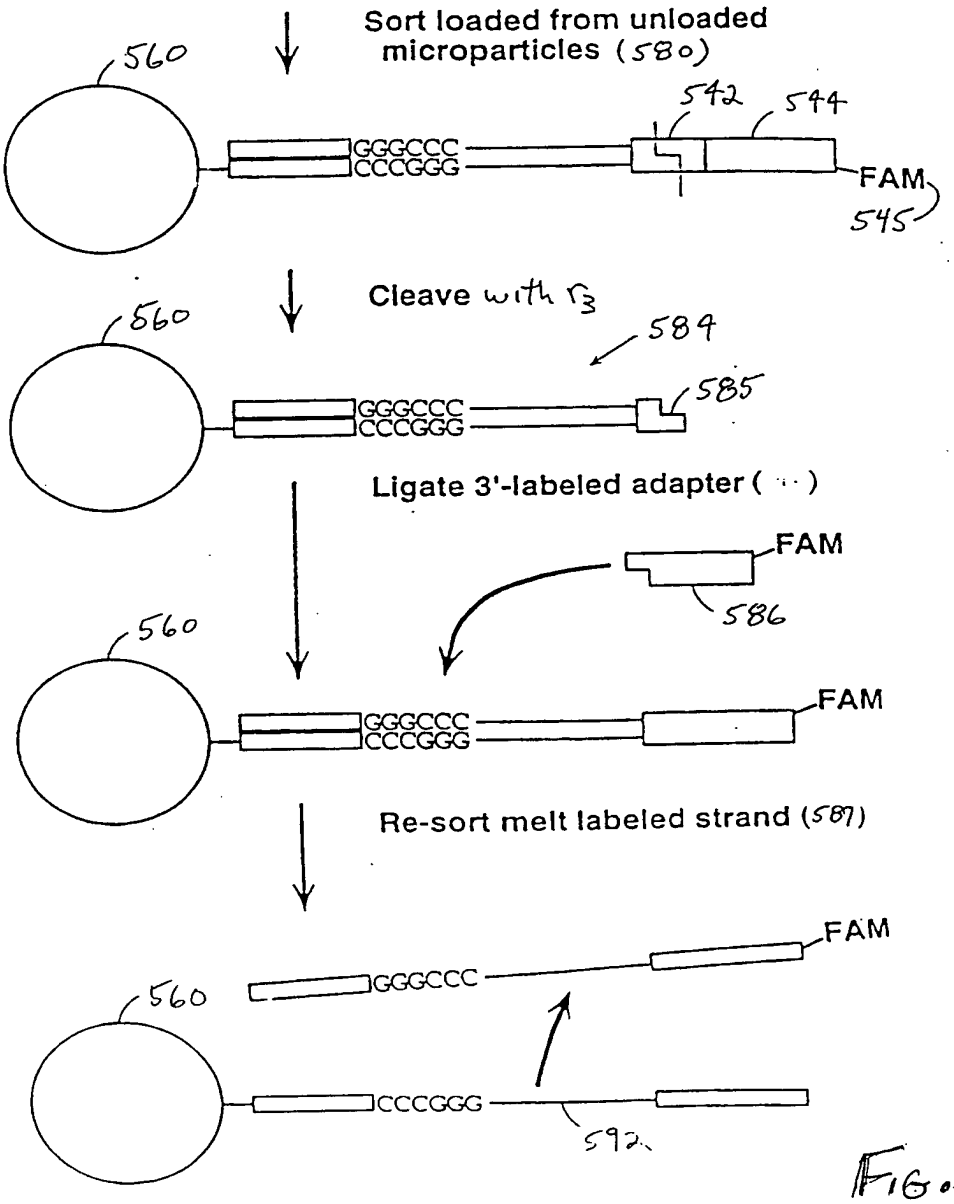

Sort loaded from unloaded microparticles (580)
560
542
544
GGGCCC
CCCGGG
FAM
545
Cleave with r3
560
584
585
GGGCCC
CCCGGG
Ligate 3'-labeled adapter ( )
FAM
586
560
FAM
GGGCCC
CCCGGG
Re-sort melt labeled strand (587)
FAM
560
GGGCCC
CCCGGG
592

FIG. 5B

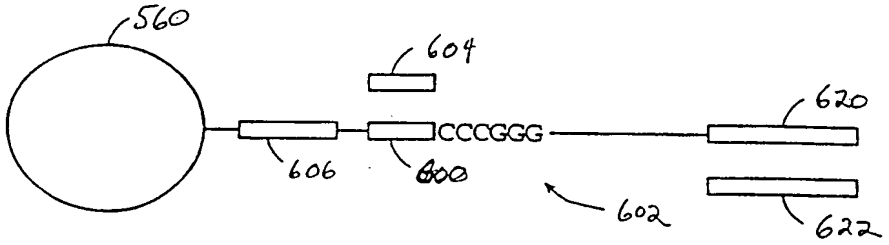

560
604
620
CCCGGG
606
600
602
622

Fig. 6A

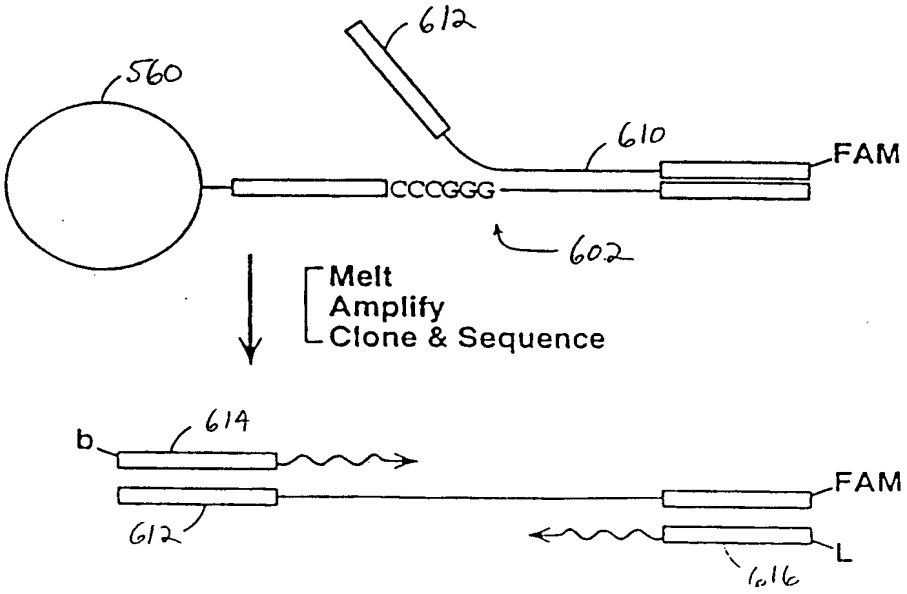
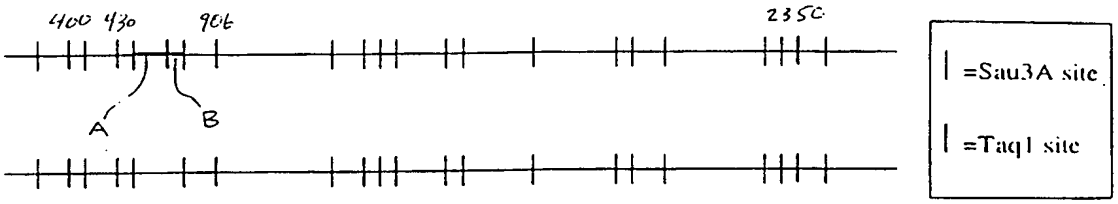
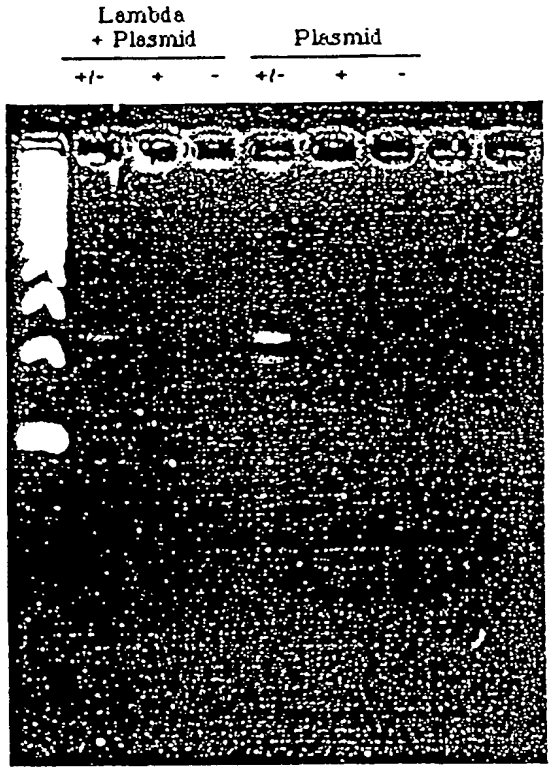

612
560
610
FAM
CCCGGG
602
Melt
Amplify
Clone & Sequence
b
614
FAM
612
L
616

Fig. 6B

Fig. 7A





Expected bands approx 190bp
230bp

Fig. 7B

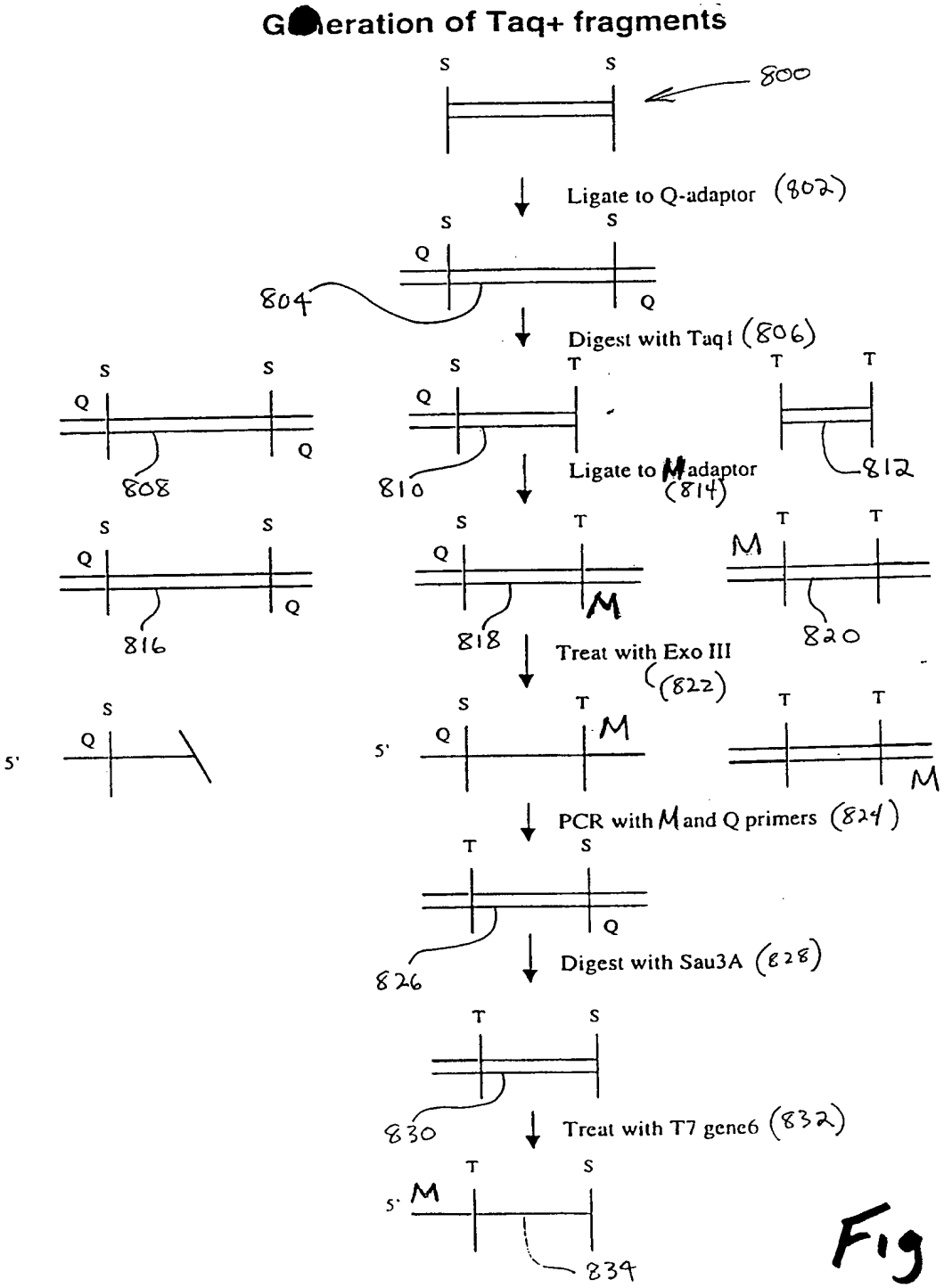

Generation of Taq+ fragments
S
S
800
Ligate to Q-adaptor (802)
Q
Q
804
Digest with Taq1 (806)
T
T
808
810
812
Ligate to M adaptor (814)
M
816
818
820
Treat with Exo III (822)
5'
826
PCR with M and Q primers (824)
Digest with Sau3A (828)
830
Treat with T7 gene6 (832)
834

Fig 8A

Generation of Taq- fragments

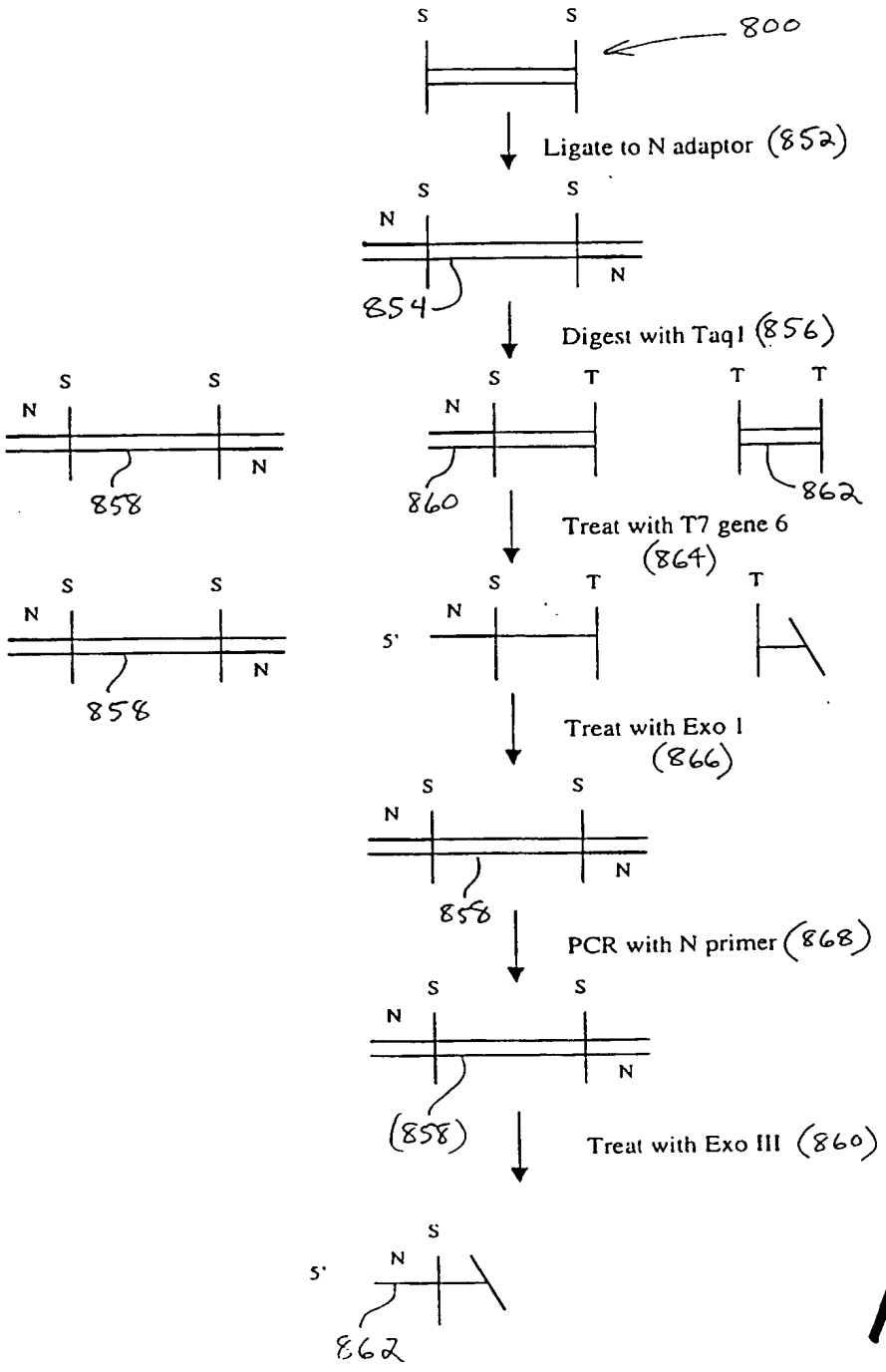


Fig 8E

Rescue of polymorphic fragments

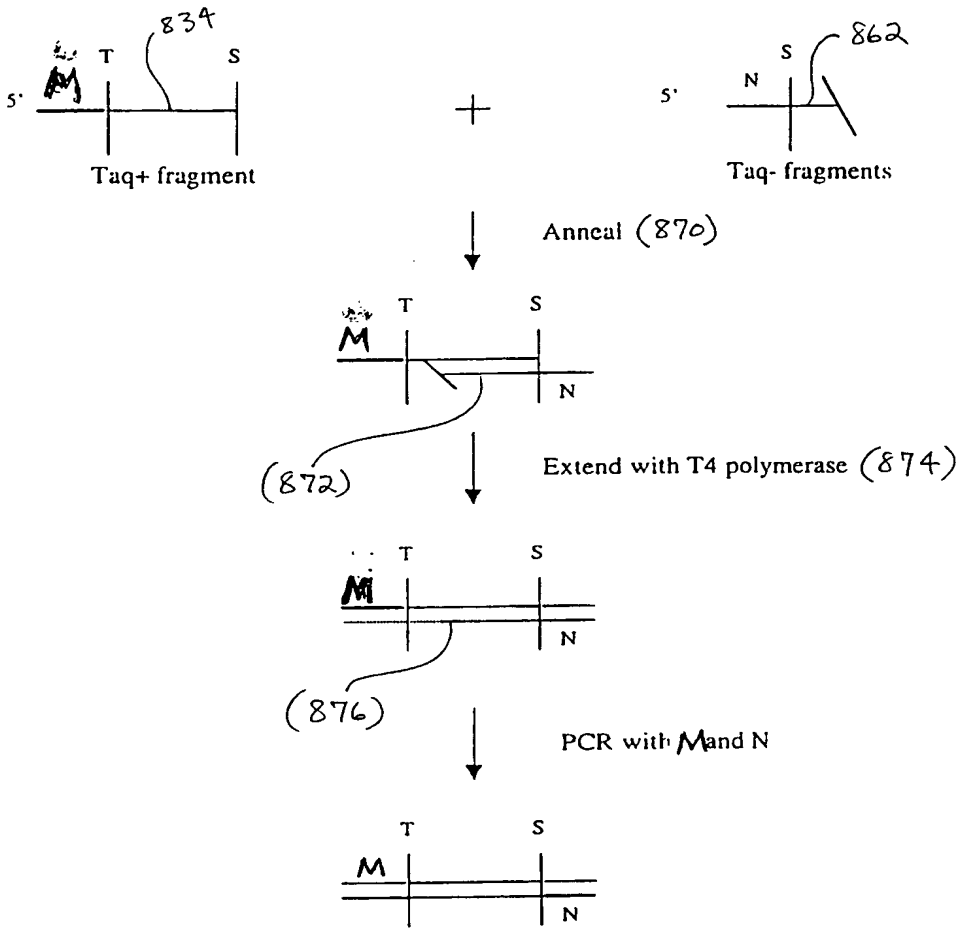


Fig 8C

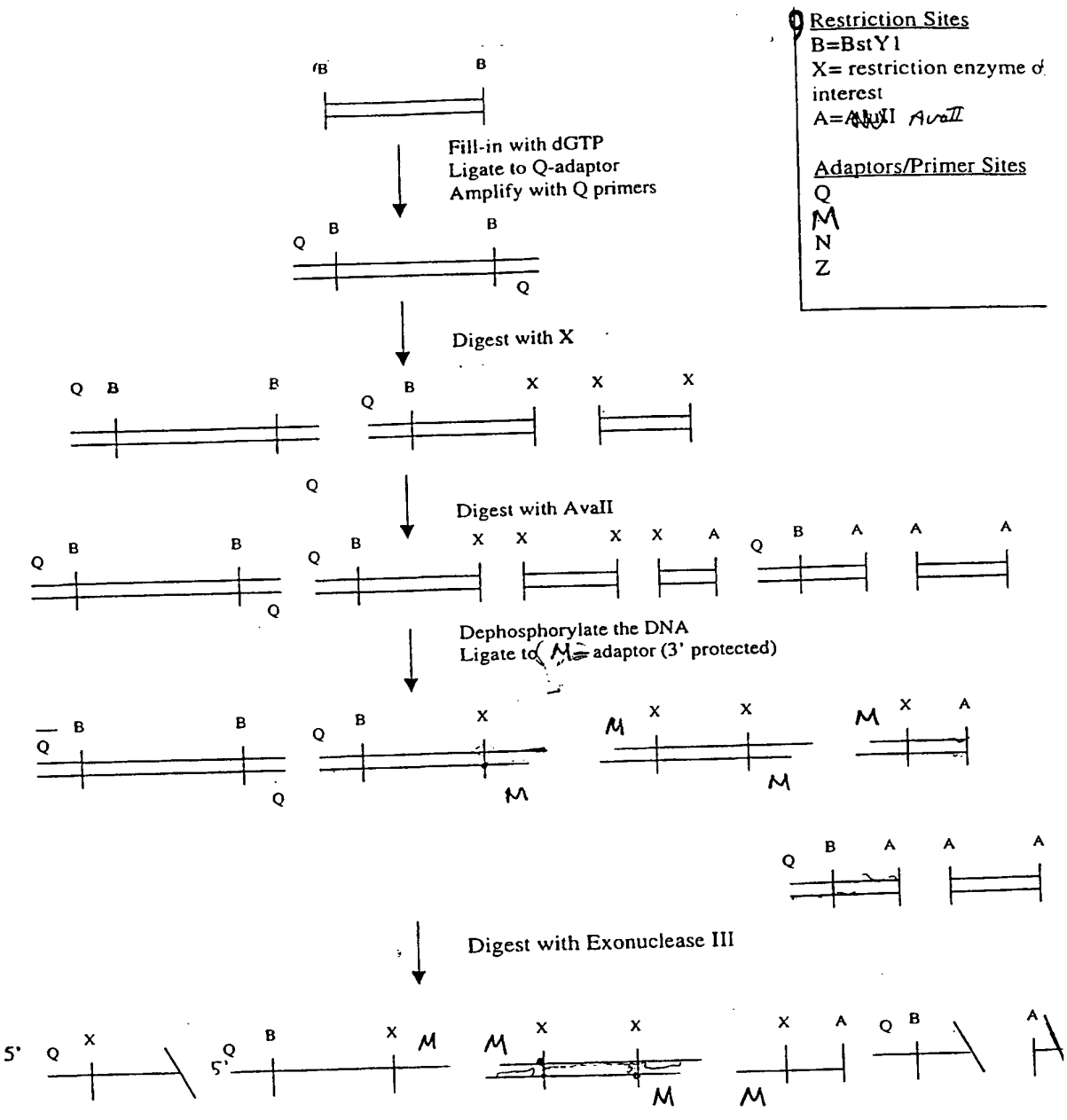

Restriction Sites
B=BstY1
X= restriction enzyme of interest
A=AluI AvaII
Adaptors/Primer Sites
Q
M
N
Z
Fill-in with dGTP
Ligate to Q-adaptor
Amplify with Q primers
Digest with X
Digest with AvaII
Dephosphorylate the DNA
Ligate to M adaptor (3' protected)
Digest with Exonuclease III
5'

Fig 9A

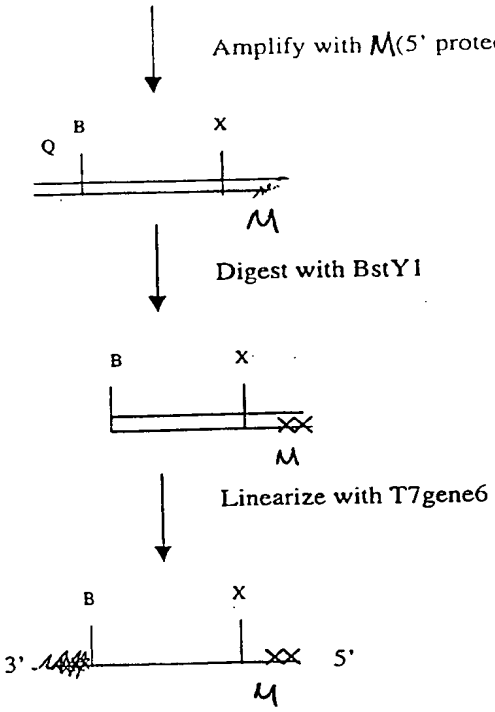

Amplify with M(5' protected) and Q primers
Q
B
X
M
Digest with BstY1
B
X
M
Linearize with T7gene6
B
X
3'
5'
M

Fig. 9B

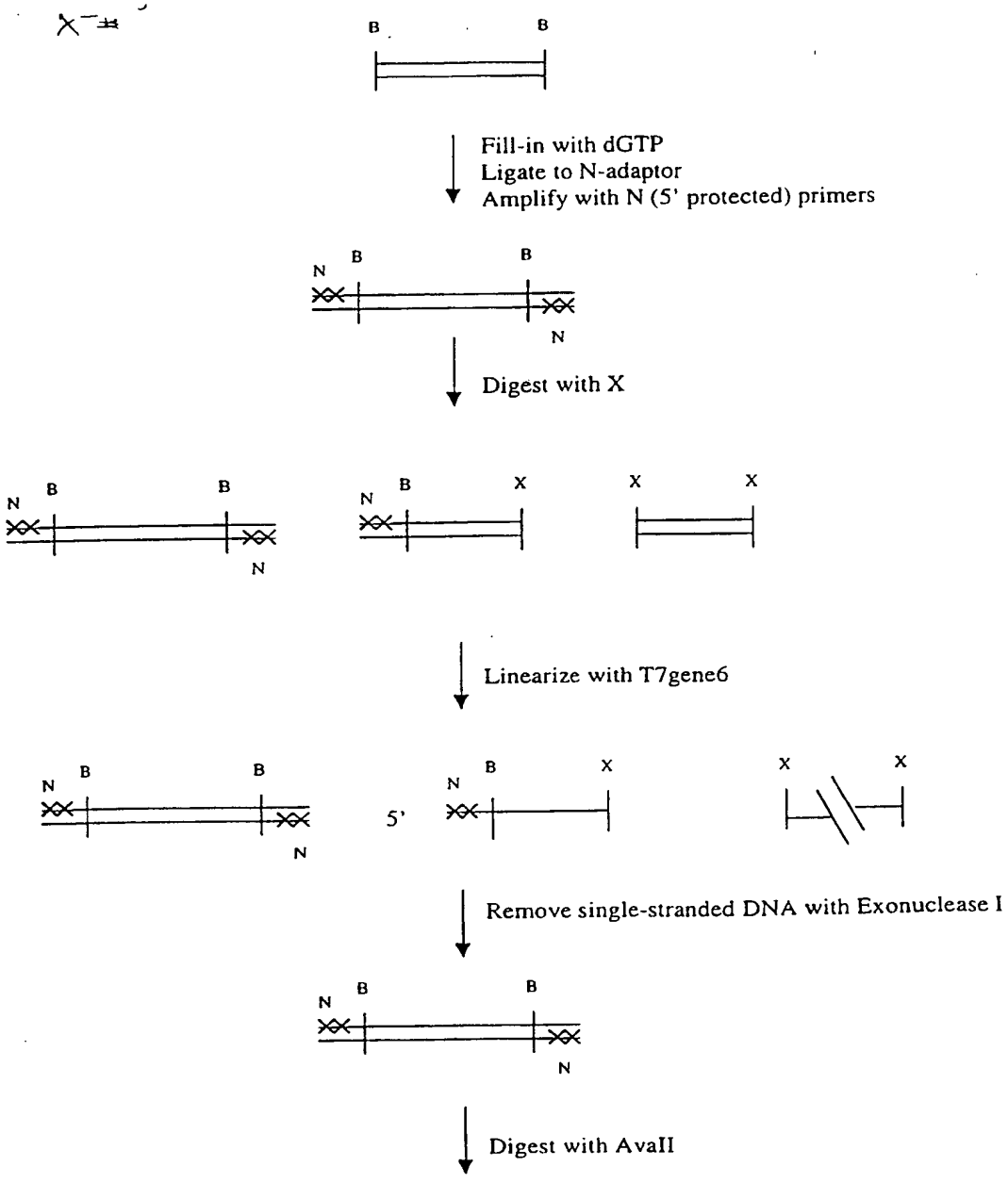

B B
Fill-in with dGTP
Ligate to N-adaptor
Amplify with N (5' protected) primers
N B B N
Digest with X
N B B N
N B X
X X
Linearize with T7gene6
N B B N
5'
N B X
X X
Remove single-stranded DNA with Exonuclease I
N B B N
Digest with AvaII

Fig 10A.

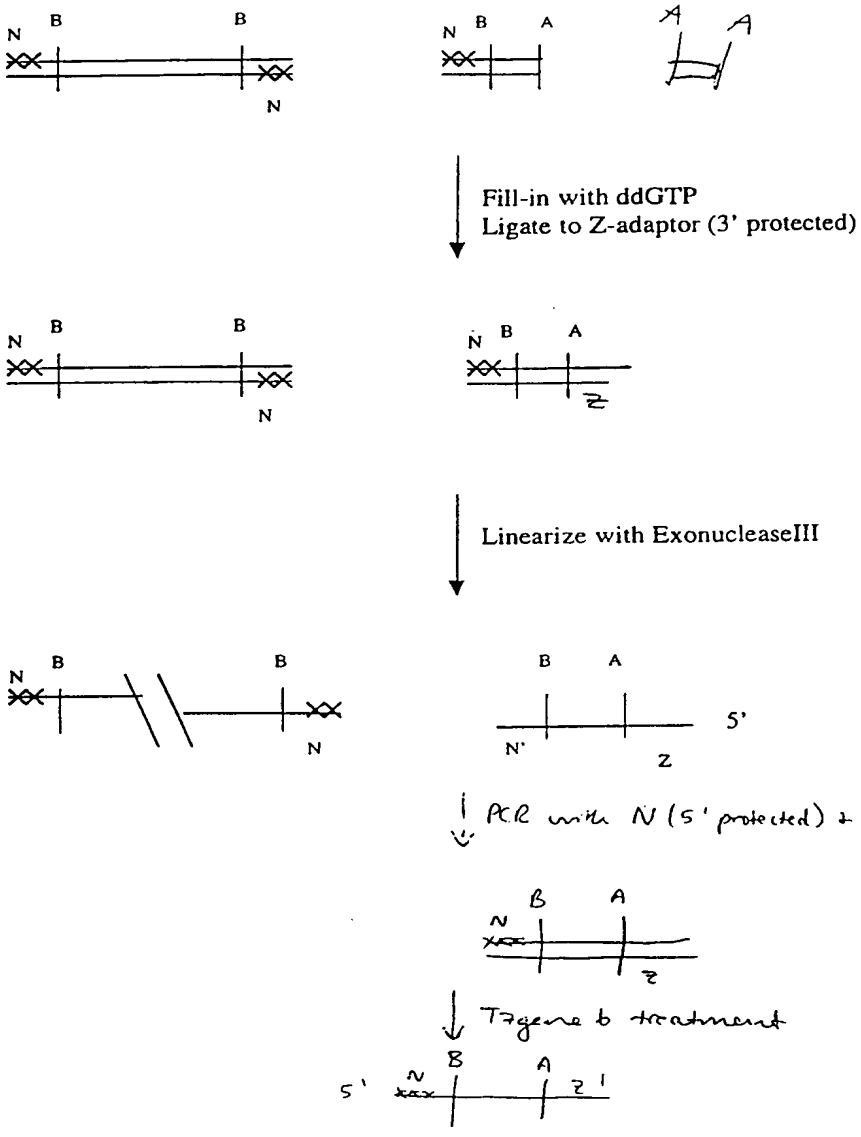

N B B N
N B A
A A
Fill-in with ddGTP
Ligate to Z-adaptor (3' protected)
N B B N
N B A Z
Linearize with ExonucleaseIII
N B B N
B A 5'
N' Z
PCR with N (5' protected) + Z
B A
N Z
Tzgene b treatment
B A
5' N Z

Fig. 10B

Figure 11

Hybridization of Tai + and Tai −